

In the Specification:

Please replace paragraph 2 at page 23 that continues over to page 24 of the specification with the following paragraph:

These fractions were freeze-dried for qualitative analysis. These two types of hEGF were analyzed for N-terminal amino acid sequence and molecular weight in the Korea Basic Science Institute. From two peaks, hEGF activity was detected. Of them, the relatively hydrophilic peak was found to have a molecular weight of 6,205 as measured by MALDI-Mass analysis. Therefore, it was a complete hEGF consisting of 53 amino acid residues. On the other hand, the hEGF of the relatively hydrophobic peak, eluted at a higher acetonitrile concentration, was measured to be 6,053 in molecular weight with 52 amino acid residues. Amino acid sequencing analysis read a sequence of Asn-Ser-Asp-Ser-Glu- (SEQ ID NO:10) in the N-terminal region of both the two types of hEGF, revealing that both hEGF molecules are separated accurately from the signal peptide by KEX2. Therefore, the hEGF consisting of 52 amino acid residues resulted from the separation of one amino acid residue from the C-terminal of the whole hEGF. That is, since the whole hEGF has a sequence of -Trp-Trp-Glu-Leu-Arg (SEQ ID NO:11) in its C-terminal region, the separation of the arginine residue from the full-length hEGF makes the resulting hEGF of 52 amino acid residues more hydrophobic.